

## FIG. 1B

1 GTTTTCAAAA TCGGTGGAGG TGCATGAAAA AGTTATT	1	AGTTATTGO	166
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- 41 CATTTTTGA AAATAAAAA ATATCAATAA GTTGGAGTCA ↓START
- 81 TTACCGAATT TTTATACTTA TTTGTTTAGA ATGAACTTTA
  -35
  -10
- 121 TAACATAGTT GGATAGAGTT TTCGATTTAA TACATTAAAT
- 161 GTGAACCTTG CTACAACAAG ATGTGCATCA GA<u>AGGAGTGG</u>
  RIBOSOME BINDING SITE
- 201 TTTAATAATG --sarR--TAA (SEQ ID NO:19)

## FIG. 1C

10 20 30 40
SarR M--SKINDINDLVNATFQVKKFFRDTKKKFNLNYEEIYILN
: .::: .:. : : :::: ::: :::
SarA MAITKINDCFELLSMVTYADKLKSLIKKEFSISFEEFAVLT

SarR IKN (SEQ ID NO:2)

SarA IEL (SEQ ID NO:3)

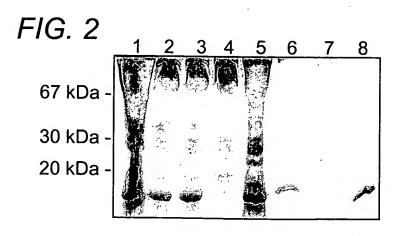


FIG. 3A

FIG. 3B

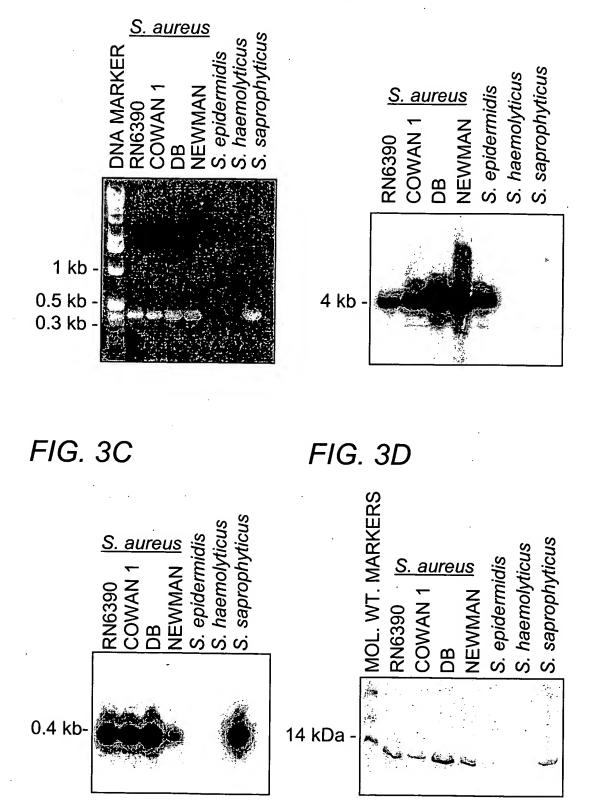


FIG. 4A

FIG. 4B

Sar P1

+

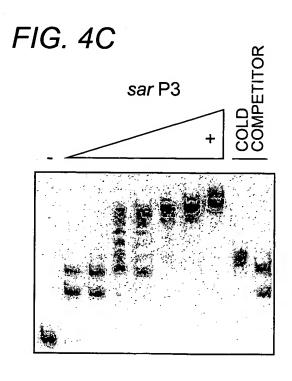
COFD

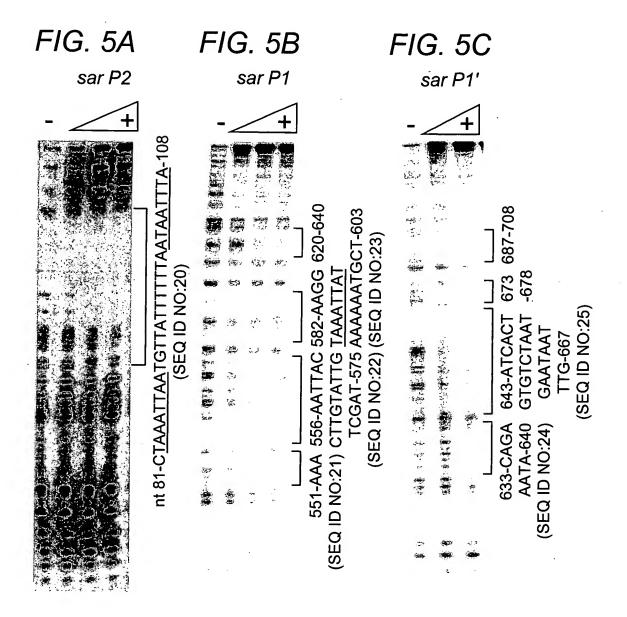
COFD

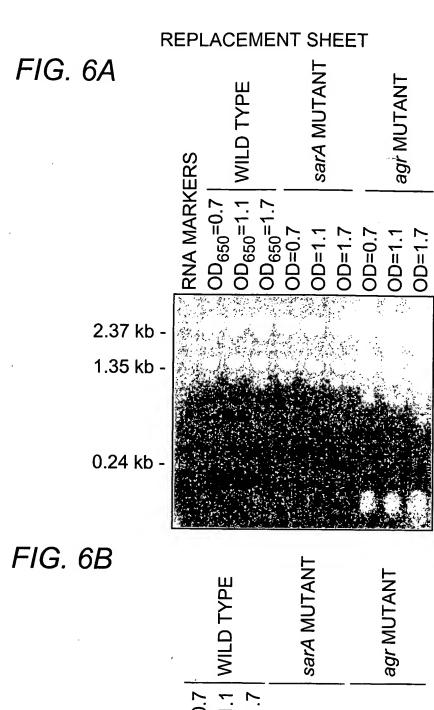
COFD

A

FIG. 4B







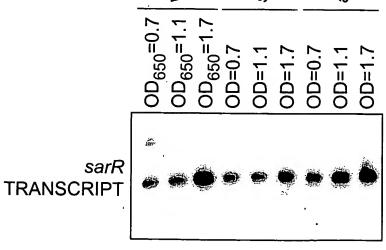


FIG. 6C

OD650nm=1.1 | SarK | OD650nm=1.7 | OD650nm=1.7 | OD650nm=1.7 | CONTROL

FIG. 7A

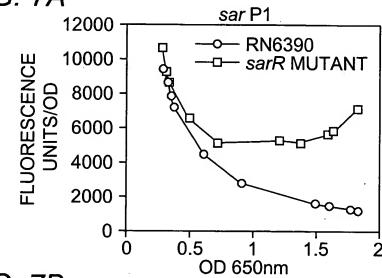


FIG. 7B

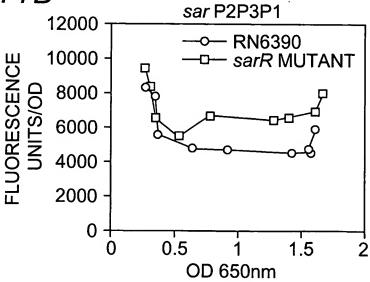


FIG. 8A

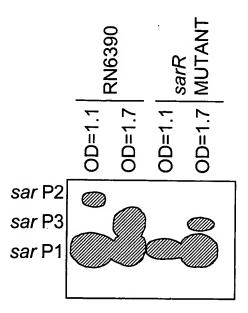


FIG. 8B

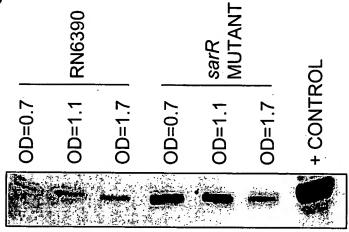
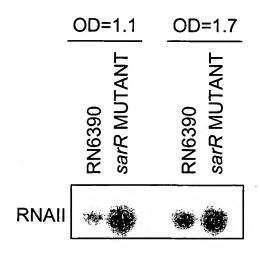


FIG. 8C



# FIG. 9A

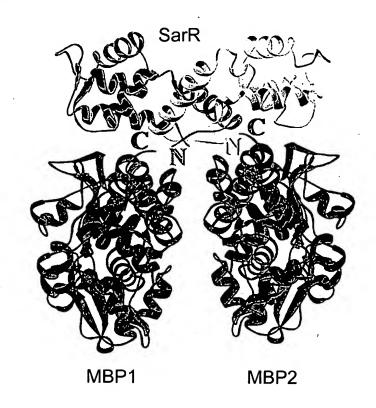
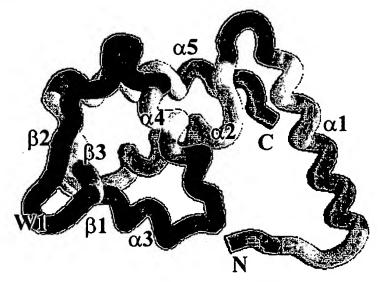
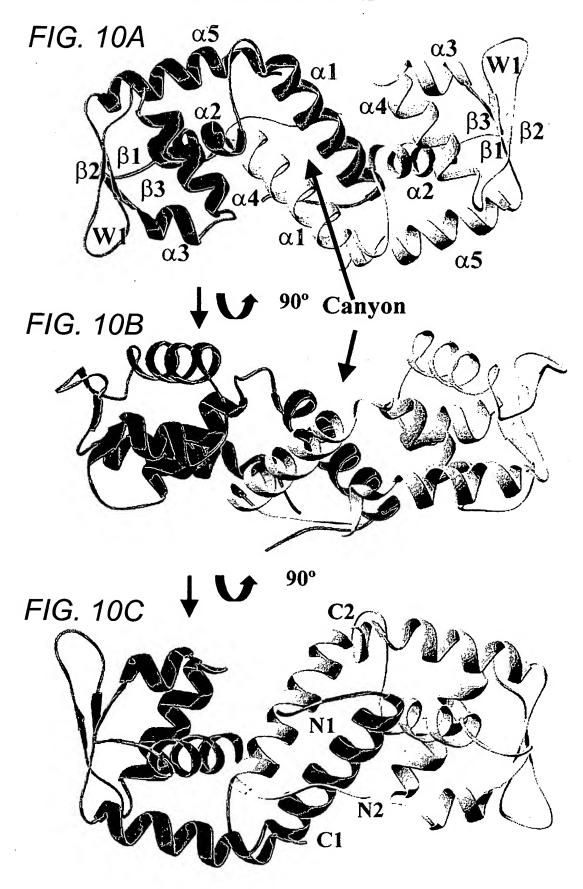
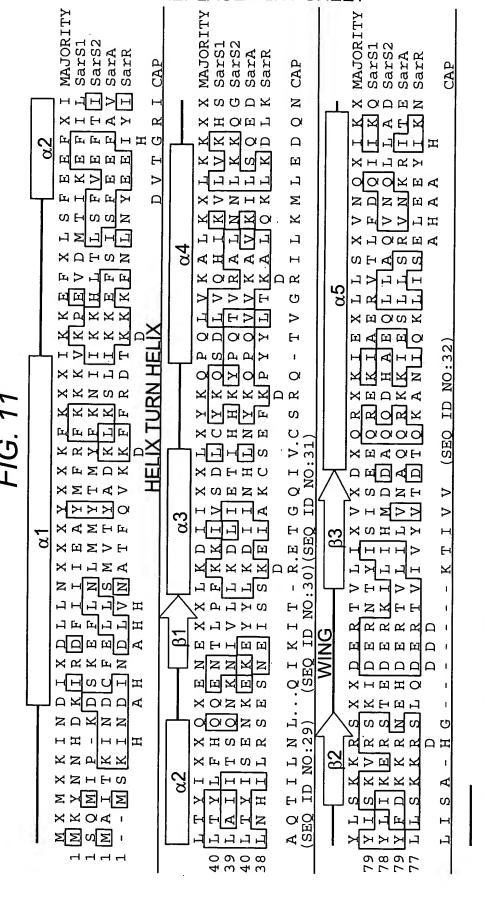


FIG. 9B







MAJORITY SarS1 SarS2 SarA SarR NO:26) NO:27) NO:28) NO:35) NO:2) 88888 SEQ SEQ SEQ SEQ SEQ X I DZ I ZZMZ : 1119 1118 1119

## FIG. 12A



FIG. 12B

